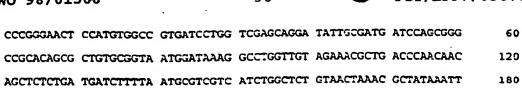
SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: LONZA AG
 - (B) STREET: Muenchensteinerstrasse 38
 - (C) CITY: Basle
 - (E) COUNTRY: Switzerland
 - (F) POSTAL CODE: 4002
 - (ii) TITLE OF INVENTION: Process for the preparation of (S) - or (R) -3,3,3-trifluoro-2hydroxy-2-methylpropionic acid
 - (iii) NUMBER OF SEQUENCES: 14
 - (iv) COMPUTER-READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (c) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: Genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: Klebsiella oxytoca
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (vii) PROVENANCE:
 - (B) CLONE(S): pPRS2a
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: join(197..1181)
 - (D) OTHER INFORMATION:/product= "amidase"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

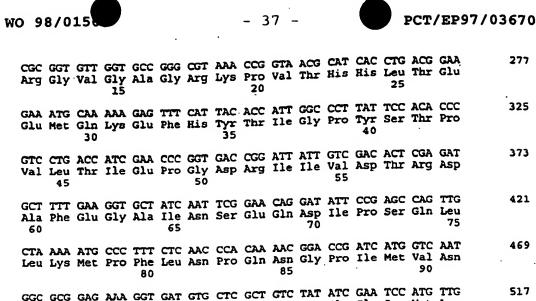
229



ACGTGGAGAA TAACAT ATG AAA TGG TTG GAA GAA TCC AT? ATG GCC AAA Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys

949

997



GGC GCG GAG AMA GGT GAT GTG CTC GCT GTC TAT ATC GAA TCC ATG TTG Gly Ala Glu Lys Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu CCC CGC GGC GTT GAT CCC TAC GGC ATC TGC GCC ATG ATT CCG CAT TTT Pro Arg Gly Val Asp Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe 565 GGC GGA CTG ACC GGG ACC GAC CTG ACG GCC ATG CTC AAT GAT CCG CTG 613 Gly Gly Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu CCA GAA AAG GTG CGC ATG ATT AAA CTC GAC AGT GAA AAG GTC TAC TGG 661 Pro Glu Lys Val Arg Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Tro AGC ARA CGC CAT ACG CTT CCC TAT ARA CCC CAT ATT GGC ACC TTG AGC 709 Ser Lys Arg His Thr Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser GTA TCG CCA GAA ATT GAC TCA ATC AAT TCA CTG ACG CCA GAC AAT CAC 757 Val Ser Pro Glu Ile Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His 180 GGC GGG AAT ATG GAT GTG CCG GAT ATA GGA CCA GGG AGT ATT ACC TAT Gly Gly Asn Met Asp Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr 805 195 CTG CCG GTA CGT GCG CCT GGA GGC CGC CTG TTT ATT GGT GAT GCC CAT Leu Pro Val Arg Ala Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His 853 GCT TGT CAG GGT GAT GGT GAG ATT TGC GGG ACC GCA GTA GAG TTT GCC Ala Cys Gln Gly Asp Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala 901

TCA ATC ACC ACC ATC AAA GTC GAT TTG ATC AAG AAC TGG CAG CTT TCC

Ser Ile Thr Thr Ile Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser

TGG CCA CGA ATG GAG AAT GCC GAA AAT ATT ATG AGT ATT GGC AGT GCA

Trp Pro Arg Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala 260



CGT CCG CTG GAG GAT GCG ACG CGA ATT GCA TAT CGC GAC TTA ATT TAC Arg Pro Leu Glu Asp Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr 270 275 280	1045
TGG CTG GTA GAA GAC TTT GGC TTC GAA CAA TGG GAT GCC TAC ATG CTT TTP Leu Val Glu Asp Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu 285 290 295	1093
CTG AGT CAA TGC GGC AAA GTG CGG CTG GGC AAC ATG GTC GAC CCC AAA Leu Ser Gln Cys Gly Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys 300 305 315	1141
TAC ACC GTT GGC GCG ATG CTG AAC AAA AAC CTG TTA GTT TAGTAGGAAT Tyr Thr Val Gly Ala Met Leu Asn Lys Asn Leu Leu Val 320 325	1190
AACTAACCGG TGAACATTAC CCGGATGTAG ATCGGGGTAA TGTGTAAGTT CAAACAATCG	1250
CTATTTTTAA CAGCTAAAGC AGGTGCATAT GGGGCCAGAT ACACCCATCA ATATTGGTTT	1310
ACTITACTCC TICAGCGGAG TGACGGCGGC ACAAGAGTTG TCACAATGGC GCGGAGCAAC	1370
CCAGGCTATT GCCGAAATTA ATCAAAATGG CGGCATCAAC GGCAGACCAC TCAATGCAAT	1430
TCATTTGGAT CC	1442

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala 1 5 10 15

Gly Arg Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys Glu 20 25 30

Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile Glu 35 40

Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp Ala Phe Glu Gly Ala 50 55 60

Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu Leu Lys Met Pro Phe 65 70 75 80

Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala Glu Lys Gly 85 90 95

Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg Gly Val Asp
100 105 110

Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe Gly Gly Leu Thr Gly 115 120 125

Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu Pro Glu Lys Val Arg 130 135 140



Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp Ser Lys Arg His Thr 145 150 150 160

Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser Val Ser Pro Glu Ile 165 170 -175

Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His Gly Gly Asn Met Asp 180 185

Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr Leu Pro Val Arg Ala

Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His Ala Cys Gln Gly Asp 210 225

Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala Ser Ile Thr Thr Ile 225 230 235 240

Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser Trp Pro Arg Met Glu 245 250 255

Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg Pro Leu Glu Asp 260 265 270

Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr Trp Leu Val Glu Asp 275 280 285

Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu Leu Ser Gln Cys Gly 290 295

Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys Tyr Thr Val Gly Ala 305 310 315

Met Leu Asn Lys Asn Leu Leu Val

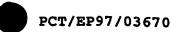
- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

 Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala

 1 10 15

Ser Arg Lys Pro

- (2) INFORMATION FOR SEQ ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known



- (ii) MOLECULE TYPE: peptide
- (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Tyr Trp Ser Lys

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys 5

- (2) INFORMATION FOR SEQ ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Thr Val Gly Ala Met Leu Asn Lys

- (2) INFORMATION FOR SEQ ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known



- (D) TOPOLOGY: not known
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

 Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg

 1 10
- (2) INFORMATION FOR SEQ ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Trp Leu Glu Glu Ser Ile Met Ala Lys 1 5

- (2) INFORMATION FOR SEQ ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala 1 5 10 15

Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid



- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: Asp Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln 10

Leu Leu Lys

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: Glu Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile

Glu Pro Gly Asp Arg 20

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: Leu Phe Ile Gly Asp Ala His Ala Glu Gln Gly Asp Gly Glu Ile Glu
- 1 5 10 15

Gly Thr Ala Val Glu Phe Ala 20



- INFORMATION FOR SEQ ID NO: 13: (2)
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg

- (2) INFORMATION FOR SEQ ID NO: 14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known
 - (ii) MOLECULE TYPE: peptide
 - (vi) ORIGIN:
 - (C) INDIVIDUAL/ISOLATE: PRS1
 - (vii) PROVENANCE:
 - (B) CLONE(S): PRS1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14: Gly Val Asp Pro Tyr Gly Ile Glu Ala Met Ile Pro His Phe Gly Gly

Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Gin Leu Gin Pro

Lys